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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/761,640	01/18/2001	Ming-Hui Wei	CL000964-CIP	6098

25748 7590 12/10/2004

CELERA GENOMICS CORP.
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EXAMINER	
NGUYEN, QUANG	
ART UNIT	PAPER NUMBER
1636	

DATE MAILED: 12/10/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/761,640	WEI ET AL.	
	Examiner	Art Unit	
	Quang Nguyen, Ph.D.	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *02 September 2004*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *4,8,9 and 24-30* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *4,8,9 and 24, 27-30* is/are rejected.

7)☒ Claim(s) *25 and 26* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *attached sequence search*.

DETAILED ACTION

Applicants' amendment filed on 9/2/04 has been entered.

Amended claims 4, 8-9 and 24-30 are pending in the present application, and they are examined on the merits herein.

Sequence Compliance

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth below.

Specifically, Figures 2-3 disclose numerous nucleotide and amino acid sequences that have not been assigned with any SEQ ID NO., either in the Figures or in the section of Description of the Figure Sheets. Some of the disclosed sequences are not even listed in either a Paper Sequence Listing or in a CRF. This sequence non-compliance does not affect the nature of the claims being examined on the merits herein. Failure to comply with the sequence rule will be deemed as non-responsive in the reply to this Office Action.

Specification

The disclosure is objected to because in the section of Description of the Figure Sheets, the sequences referred as SEQ ID Nos: 4, 6 in Figure 1; SEQ ID Nos 2, 7 in Figure 2 and SEQ ID NO: 3 in Figure 3 do not match with the sequences with the

corresponding SEQ ID Nos in the sequence listing. Please also correct similar mistakes throughout the specification.

Appropriate correction is required.

Claim Objections

Amended claim 4 is objected to because SEQ ID NO:1 is identical to SEQ ID NO:7 (see Sequence listing), and therefore it is an improper Markush claim. Appropriate correction is required.

Amended claim 26 is objected to under 37 CFR 1.75 as being a substantial duplicate of claim 25. When two claims in an application are duplicates or else are so close in content that they both cover the same thing, despite a slight difference in wording, it is proper after allowing one claim to object to the other as being a substantial duplicate of the allowed claim. See MPEP § 706.03(k). This is because SEQ ID NO:1 is identical to SEQ ID NO:7 (see Sequence listing).

Response to Amendment

The rejections under 35 U.S.C. 101 and 112, 1st paragraph were withdrawn.

With respect to claimed embodiments specifically reciting SEQ ID NO:4 in newly amended claims, following are new grounds of rejections.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
>
> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 4, 8-9, 24, 27 and 30 are rejected under 35 U.S.C. 102(b) as being anticipated by Stork et al. (WO 97/00315). **This is a new ground of rejection necessitated by Applicants' amendment.**

The claims are drawn to an isolated nucleic acid molecule encoding a phosphatase protein consisting of a nucleotide sequence that encodes a protein comprising an amino acid sequence of SEQ ID NO:4, a nucleic acid vector, an isolated host cell comprising the same, its complementary sequence strand, and a process for producing a polypeptide by culturing the same host cell.

Stork et al. disclose a cDNA sequence encoding a mitogen-activated protein kinase phosphatase MKP-2 that contains the same Val-Leu-Val-His-Cys sequence as that of SEQ ID NO:4 of the presently claimed invention (see Figure 22), and therefore the reference meets the limitation of a protein comprising an amino acid sequence of SEQ ID NO:4. Stork et al. further teach to clone the cDNA sequence in plasmid vectors to produce over-expressing stable cell lines (see example 2), as well as a method of

recovering MKP-2 protein in substantially pure form by cells expressing MKP-2 protein (page 8, line 32 continues to line 3 of page 9; page 9, lines 20-27). Please also note that a cDNA molecule contains both sense and its completely complementary anti-sense strand.

Accordingly, the teachings of Stork et al. meet every limitation of the instant claims. Therefore, Stork et al. anticipate the instant claims.

Claims 4, 8-9, 24 and 27-30 are rejected under 35 U.S.C. 102(e) as being anticipated by Luche et al. (US Patent 6,825,021). **This is a new ground of rejection necessitated by Applicants' amendment**.

Luche et al. disclose a cDNA sequence encoding a murine dual-specificity phosphatase DSP-15 polypeptide that has the same amino acid sequence of SEQ ID NO :4 (see Figures 4-5 and the attached sequence search). Luche et al. further teach a method for producing a DSP-15 polypeptide, comprising the steps of: (a) culturing a host cell transformed or transfected with an expression vector encoding DSP-15 polypeptide under conditions that permit expression of the DSP-15 polypeptide; and (b) isolating DSP-15 polypeptide from the host cell culture (col. 2, lines 9-42). Host cells include prokaryotes, yeasts and mammalian cells (col. 8, lines 4-24). The polynucleotide is cloned into vectors such as plasmids, phagemids, lambda phage derivatives, cosmids, viral vector and others (col. 12, lines 16-44), and an expression vector contains a promoter operatively linked to a polynucleotide of interest, for this instance a polynucleotide encoding a DSP-15 polypeptide (e.g., see example 3).

Please also note that a cDNA molecule contains both sense and its completely complementary anti-sense strand.

Accordingly, the teachings of Luche et al. meet every limitation of the instant claims. Therefore, Luche et al. anticipate the instant claims.

Examiner notes that the teachings of Luche et al. (US Patent 6,825,021) are identical to the teachings of WO 02/24720 A2 (IDS).

Examiner further notes that WO 01/2004 A2 (with a priority date of 15 September 1999) is also pertinent to the present application. However, the publication is not applied as a prior art because its publication date is 14 September 2000.

In light of the teachings of Luche et al. (US Patent 6,825,021) and WO 01/2004 A2, it is apparent that the encoded amino acid sequence of SEQ ID NO:4 of the presently claimed invention is recognized as a phosphatase protein.

Conclusion

As noted in the previous Office action mailed on 8/27/03, the prior art does not teach or fairly suggest a nucleic acid molecule of SEQ ID NO:1, a vector or an isolated host cell comprising the same as well as a method for producing a polypeptide by culturing the same isolated host cell.

No claims are allowed.

Claims 25 and 26 are objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL.** See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Quang Nguyen, Ph.D., whose telephone number is (571) 272-0776.

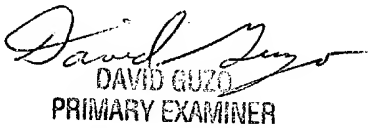
If attempts to reach the examiner by telephone are unsuccessful, the examiner's mentor, David Guzo, Ph.D., may be reached at (571) 272-0767, or SPE, Irem Yucel, Ph.D., at (571) 272-0781.

To aid in correlating any papers for this application, all further correspondence regarding this application should be directed to Group Art Unit 1636; Central Fax No. (703) 872-9306.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

Quang Nguyen, Ph.D.



DAVID GUZO
PRIMARY EXAMINER

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23	687	28.2	409	24	ABL40802	Human MAP kinase p
24	648	26.6	1348	22	AAH99712	Human protein enco
25	591.5	24.3	426	24	ABL40800	Human MAP kinase p
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ALIGNMENTS

RESULT 1
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AC AAD36063;
XX
DT 09-AUG-2002 (first entry)
XX
DE Murine dual-specificity phosphatase 15 (DSP-15) cDNA.
XX
KW Murine; dual-specificity phosphatase 15; DSP15; antiallergic; cytostatic;
KW immunosuppressive; MAP; mitogen activated protein kinase; cancer; enzyme;
KW signal transduction; cell proliferation; Duchenne muscular dystrophy;
KW cell cycle abnormality; graft-versus-host disease; autoimmune disease;
KW metabolic disease; allergy; screening; gene; ss.
XX
OS Mus musculus.
XX

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PR   18-SEP-2001; 2001US-0955732.
XX
PA   (CEPT-) CEPTYR INC.
XX
PI   Luche RM,  Wei B;
XX
DR   WPI; 2002-394127/42.
DR   P-PSDB; AAE22733.
XX
PT   New dual-specificity phosphatase 15 polypeptide and polynucleotides,
PT   useful for treating e.g. Duchenne muscular dystrophy, cancer,
PT   graft-versus-host disease, autoimmune diseases, allergies, metabolic
PT   diseases
XX
PS   Claim 56; Fig 4; 91pp; English.
XX
CC   The invention relates to a new isolated dual-specificity phosphatase 15
CC   (DSP-15) polypeptide which retains the ability to dephosphorylate an
CC   activated MAP (mitogen activated protein) kinase. DSPs are phosphatases
CC   that dephosphorylate both phosphotyrosine and phosphothreonine/serine
CC   residues. DSP-15 polypeptides may be used to identify agents that
CC   modulate DSP-15 activity, where such agents may inhibit or enhance signal
CC   transduction via a MAP-kinase cascade, leading to cell proliferation. DSP
CC   polypeptides, modulating agents, and/or polynucleotides encoding the
CC   polypeptides may be used to modulate DSP-15 activity in a patient, and to
CC   ameliorate disorders such as Duchenne muscular dystrophy, cancer, graft-
CC   versus-host disease, autoimmune diseases, allergies, metabolic diseases,
CC   abnormal cell growth, abnormal cell proliferation and cell cycle
CC   abnormalities. DSP-15 alternate form polypeptides are useful in screening
CC   assays for modulators of enzyme activity and/or substrate binding. The
CC   present sequence is murine DSP-15 cDNA.
XX
SQ   Sequence 2618 BP; 538 A; 857 C; 769 G; 454 T; 0 other;
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US-09-761-640-4 (1-471) x AAD36063 (1-2618)

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Qy     121 ArgProProArgLeuArgTyrLeuLeuValValSerThrArgGluGlyGluGlyLeuSer 140
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Qy     141 GlnAspGluThrValLeuLeuGlyValAspPheProAspSerSerSerProSerCysThr 160
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Qy     161 LeuGlyLeuValLeuProLeuTrpSerAspThrGlnValTyrLeuAspGlyAspGlyGly 180
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Db     515 CTGGGCCTGGTCTTGCCCCTCTGGAGTGACACCCAGGTGTACTTAGATGGAGACGGGGGC 574

Qy     181 PheSerValThrSerGlyGlyGlnSerArgIlePheLysProIleSerIleGlnThrMet 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     201 TrpAlaThrLeuGlnValLeuHisGlnAlaCysGluAlaAlaLeuGlySerGlyLeuVal 220
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Db     635 TGGGCCACACTCCAGGTATTGCACCAAGCATGTGAGGCAGCTCTAGGCAGCGGCCTTGTA 694

Qy     221 ProGlyGlySerAlaLeuThrTrpAlaSerHisTyrGlnGluArgLeuAsnSerGluGln 240
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Db     695 CCGGGTGGCAGTGCCCTCACCTGGGCCAGCCACTACCAGGAGAGACTGAACTCCGAACAG 754

Qy     241 SerCysLeuAsnGluTrpThrAlaMetAlaAspLeuGluSerLeuArgProProSerAla 260
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Db     755 AGCTGCCTCAATGAGTGGACGGCTATGGCCGACCTGGAGTCTCTGCGGCCTCCCAGCGCC 814

Qy     261 GluProGlyGlySerSerGluGlnGluGlnMetGluGlnAlaIleArgAlaGluLeuTrp 280
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Db     815 GAGCCTGGCGGGTCCTCAGAACAGGAGCAGATGGAGCAGGCGATCCGTGCTGAGCTGTGG 874

Qy     281 LysValLeuAspValSerAspLeuGluSerValThrSerLysGluIleArgGlnAlaLeu 300
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Db     875 AAAGTGTTGGATGTCAGTGACCTGGAGAGTGTCACTTCCAAAGAGATCCGCCAGGCTCTG 934

Qy     301 GluLeuArgLeuGlyLeuProLeuGlnGlnTyrArgAspPheIleAspAsnGlnMetLeu 320
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Db     935 GAGCTGCGCCTGGGGCTCCCCCTCCAGCAGTACCGTGACTTCATCGACAACCAGATGCTG 994

Qy     321 LeuLeuValAlaGlnArgAspArgAlaSerArgIlePheProHisLeuTyrLeuGlySer 340
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Db     995 CTGCTGGTGGCACAGCGGGACCGAGCCTCCCGCATCTTCCCCCACCTCTACCTGGGCTCA 1054

Qy     341 GluTrpAsnAlaAlaAsnLeuGluGluLeuGlnArgAsnArgValThrHisIleLeuAsn 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1055 GAGTGGAACGCAGCAAACCTGGAGGAGCTGCAGAGGAACAGGGTCACCCACATCTTGAAC 1114

Qy     361 MetAlaArgGluIleAspAsnPheTyrProGluArgPheThrTyrHisAsnValArgLeu 380
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Qy     381 TrpAspGluGluSerAlaGlnLeuLeuProHisTrpLysGluThrHisArgPheIleGlu 400
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Qy     401 AlaAlaArgAlaGlnGlyThrHisValLeuValHisCysLysMetGlyValSerArgSer 420
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Db    1235 GCTGCAAGAGCACAGGGCACCCACGTGCTGGTCCACTGCAAGATGGGCGTCAGCCGCTCA 1294

Qy     421 AlaAlaThrValLeuAlaTyrAlaMetLysGlnTyrGluCysSerLeuGluGlnAlaLeu 440
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Qy     441 ArgHisValGlnGluLeuArgProIleAlaArgProAsnProGlyPheLeuArgGlnLeu 460
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```

```
Db   1355 CGCCACGTGCAGGAGCTCCGGCCCATCGCCCGCCCCAACCCTGGCTTCCTGCGCCAGCTG 1414

Qy    461 GlnIleTyrGlnGlyIleLeuThrAlaArgThr 471
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Db   1415 CAGATCTACCAGGGCATCCTGACGGCCAGAACC 1447

RESULT 2
ABQ73249
ID   ABQ73249 standard; cDNA; 2704 BP.
XX
AC   ABQ73249;
XX
DT   30-SEP-2002  (first entry)
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DE   Human MAP kinase phosphatase splice form 1 cDNA sequence SEQ ID NO:1.
XX
KW   Human; phosphatase; mitogen activated protein kinase phosphatase;
KW   MAP kinase; enzyme; chromosome 11; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT   CDS             94..1509
FT                   /*tag= b
FT                   /product= "MAP kinase phosphatase splice form 1"
FT   3'UTR           1510..2704
FT                   /*tag= c
XX
PN   WO200242436-A2.
XX
PD   30-MAY-2002.
XX
PF   07-NOV-2001; 2001WO-US42995.
XX
PR   20-NOV-2000; 2000US-0715177.
PR   18-JAN-2001; 2001US-0761640.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Wei M,  Ketchum KA,  Di Francesco V,  Beasley EM;
XX
DR   WPI; 2002-575237/61.
DR   P-PSDB; ABP51653.
XX
PT   Novel isolated human phosphatase peptide useful for treating disorder
PT   characterized by absence of, inappropriate or unwanted expression of
PT   the phosphatase protein, and as immunogens to raise antibodies
XX
PS   Claim 1; Fig 1A; 85pp; English.
XX
CC   The present invention describes an isolated human phosphatase peptide
CC   (I). (I) can be used for identifying a modulator of (I) by contacting
CC   (I) with an agent and determining if the agent has modulated the
CC   function or activity of (I). (I) is useful for identifying an agent that
CC   binds to (I), by contacting (I) with an agent and assaying the contacted
CC   mixture to determine whether a complex is formed with the agent bound
CC   (I). The human phosphatases from the present invention are mitogen
CC   activated protein (MAP) kinase phosphatases. These human MAP kinase
CC   phosphatases are located on chromosome 11. (I) and the polynucleotide
CC   sequences encoding (I) can be used in gene therapy. The present sequence
CC   encodes human MAP kinase phosphatase splice form 1 from the present
CC   invention.
XX
SQ   Sequence 2704 BP; 569 A; 874 C; 794 G; 467 T; 0 other;

Alignment Scores:
Pred. No.:                4.71e-195      Length:          2704
Score:                    2436.00        Matches:         471
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0

DB:                       24             Gaps:            0

US-09-761-640-4 (1-471) x ABQ73249 (1-2704)

Qy      1 MetAlaLeuValThrValSerArgSerProProGlySerGlyAlaSerThrProValGly 20
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Db     94 ATGGCCCTGGTCACAGTGAGCCGTTCGCCCCCGGGCAGCGGCGCCTCCACGCCCGTGGGG 153

Qy     21 ProTrpAspGlnAlaValGlnArgArgSerArgLeuGlnArgArgGlnSerPheAlaVal 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    154 CCCTGGGACCAGGCGGTCCAGCGAAGGAGTCGACTCCAGCGAAGGCAGAGCTTTGCGGTG 213

Qy     41 LeuArgGlyAlaValLeuGlyLeuGlnAspGlyGlyAspAsnAspAspAlaAlaGluAla 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 CTCCGTGGGGCTGTCCTGGGACTGCAGGATGGAGGGGACAATGATGATGCAGCAGAGGCC 273

Qy     61 SerSerGluProThrGluLysAlaProSerGluGluGluLeuHisGlyAspGlnThrAsp 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 AGTTCTGAGCCAACAGAGAAGGCCCCGAGTGAGGAGGAGCTCCACGGGGACCAGACAGAC 333

Qy     81 PheGlyGlnGlySerGlnSerProGlnLysGlnGluGluGlnArgGlnHisLeuHisLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 TTCGGGCAAGGATCCCAGAGTCCCCAGAAGCAGGAGGAGCAGAGGCAGCACCTGCACCTC 393

Qy    101 MetValGlnLeuLeuArgProGlnAspAspIleArgLeuAlaAlaGlnLeuGluAlaPro 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 ATGGTACAGCTGCTGAGGCCGCAGGATGACATCCGCCTGGCAGCCCAGCTGGAGGCACCC 453

Qy    121 ArgProProArgLeuArgTyrLeuLeuValValSerThrArgGluGlyGluGlyLeuSer 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 CGGCCTCCCCGGCTCCGCTACCTGCTGGTAGTTTCTACACGAGAAGGAGAAGGTCTGAGC 513

Qy    141 GlnAspGluThrValLeuLeuGlyValAspPheProAspSerSerSerProSerCysThr 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 CAGGATGAGACGGTCCTCCTGGGCGTGGATTTCCCTGACAGCAGCTCCCCCAGCTGCACC 573

Qy    161 LeuGlyLeuValLeuProLeuTrpSerAspThrGlnValTyrLeuAspGlyAspGlyGly 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 CTGGGCCTGGTCTTGCCCCTCTGGAGTGACACCCAGGTGTACTTAGATGGAGACGGGGGC 633

Qy    181 PheSerValThrSerGlyGlyGlnSerArgIlePheLysProIleSerIleGlnThrMet 200
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Db    634 TTCAGCGTGACGTCTGGTGGGCAAAGCCGGATCTTCAAGCCCATCTCCATCCAGACCATG 693

Qy    201 TrpAlaThrLeuGlnValLeuHisGlnAlaCysGluAlaAlaLeuGlySerGlyLeuVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 TGGGCCACACTCCAGGTATTGCACCAAGCATGTGAGGCAGCTCTAGGCAGCGGCCTTGTA 753

Qy    221 ProGlyGlySerAlaLeuThrTrpAlaSerHisTyrGlnGluArgLeuAsnSerGluGln 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 CCGGGTGGCAGTGCCCTCACCTGGGCCAGCCACTACCAGGAGAGACTGAACTCCGAACAG 813

Qy    241 SerCysLeuAsnGluTrpThrAlaMetAlaAspLeuGluSerLeuArgProProSerAla 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 AGCTGCCTCAATGAGTGGACGGCTATGGCCGACCTGGAGTCTCTGCGGCCTCCCAGCGCC 873

Qy    261 GluProGlyGlySerSerGluGlnGluGlnMetGluGlnAlaIleArgAlaGluLeuTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 GAGCCTGGCGGGTCCTCAGAACAGGAGCAGATGGAGCAGGCGATCCGTGCTGAGCTGTGG 933

Qy    281 LysValLeuAspValSerAspLeuGluSerValThrSerLysGluIleArgGlnAlaLeu 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 AAAGTGTTGGATGTCAGTGACCTGGAGAGTGTCACTTCCAAAGAGATCCGCCAGGCTCTG 993

Qy    301 GluLeuArgLeuGlyLeuProLeuGlnGlnTyrArgAspPheIleAspAsnGlnMetLeu 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 GAGCTGCGCCTGGGGCTCCCCCTCCAGCAGTACCGTGACTTCATCGACAACCAGATGCTG 1053

Qy    321 LeuLeuValAlaGlnArgAspArgAlaSerArgIleProHisLeuTyrLeuGlySer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 CTGCTGGTGGCACAGCGGGACCGAGCCTCCCGCATCTTCCCCCACCTCTACCTGGGCTCA 1113

Qy    341 GluTrpAsnAlaAlaAsnLeuGluGluLeuGlnArgAsnArgValThrHisIleLeuAsn 360
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2 potential auths

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 11, 2003, 00:12:38 ; Search time 887 Seconds
(without alignments)
1195.819 Million cell updates/sec

Title: US-09-761-640-4
Perfect score: 2436
Sequence: 1 MALVTVSRSPPGSGASTPVG.....PNPGFLRQLQIYQGILTART 471

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2436	100.0	2618	24	AAD36063	Murine dual-specif
2	2436	100.0	2704	24	ABQ73249	Human MAP kinase p
3	2436	100.0	2704	24	ABQ73252	Human MAP kinase p
4	2426	99.6	2718	24	AAD36061	Human dual-specifi
5	2426	99.6	2781	22	AAF30485	Human protein phos
6	2426	99.6	2852	24	ABQ73250	Human MAP kinase p
7	2061.5	84.6	2540	24	ABQ73251	Human MAP kinase p
8	1987.5	81.6	2322	24	ABL40805	Human MAP kinase p
9	1470.5	60.4	2061	24	ABN59832	Novel human coding
10	1113	45.7	6374	22	AAD09491	Human SGP006 phosp
11	1076.5	44.2	2260	22	AAD09493	Human SGP001 phosp
12	1045	42.9	1711	22	AAD12966	Human dual-specifi
13	1004.5	41.2	1771	22	AAH22966	Human phosphatase
14	980	40.2	1949	22	AAD12965	Human dual-specifi
15	918.5	37.7	4467	23	ABL10739	Drosophila melanog
16	852	35.0	3488	24	ABL57466	Human protein phos
17	793	32.6	1026	22	AAF63578	Human phosphatase
18	760.5	31.2	1755	22	AAH14722	Human cDNA sequenc
19	760.5	31.2	1755	24	ABL40801	Human MAP kinase p
c 20	733	30.1	8002	23	ABL10738	Drosophila melanog
c 21	714	29.3	717	22	AAH98183	Human EST-derived
22	689	28.3	599	24	ABL40803	Human MAP kinase p
23	687	28.2	409	24	ABL40802	Human MAP kinase p
24	648	26.6	1348	22	AAH99712	Human protein enco
25	591.5	24.3	426	24	ABL40800	Human MAP kinase p
26	589	24.2	1052	22	AAD12967	Human dual-specifi
27	568.5	23.3	571	22	AAH07057	Human cDNA clone (
28	539	22.1	969	22	AAS59843	Human novel cytoki
29	438	18.0	1450	22	AAS41387	cDNA encoding nove
30	438	18.0	1450	22	AAS34834	cDNA encoding nove
31	413	17.0	494	24	ABL40804	Human MAP kinase p
32	401	16.5	447	21	AAC75065	Human ORFX ORF620
33	357	14.7	951	21	AAZ33341	Human secreted pro
34	269	11.0	828	22	AAF63567	Murine phosphatase
35	256	10.5	901	22	AAF63576	Human phosphatase
36	256	10.5	1087	21	AAC63094	Human cellular pro
37	256	10.5	1292	23	AAS18101	Human 18221 cDNA.
38	256	10.5	1574	24	AAD23605	Human protein phos
39	235.5	9.7	1337	24	AAK99409	DNA of APP related
40	235.5	9.7	1830	21	AAC64262	Human dual-specifi
41	235.5	9.7	2192	21	AAA75672	DNA encoding a hum
42	231.5	9.5	687	22	AAF29608	Murine DSP-3 varia
43	231.5	9.5	1067	22	AAF63565	Murine phosphatase
44	227.5	9.3	2050	22	AAF63577	Human phosphatase
45	227.5	9.3	2118	22	AAF30479	Human protein phos

ALIGNMENTS

RESULT 1
AAD36063
ID AAD36063 standard; cDNA; 2618 BP.
XX
AC AAD36063;
XX
DT 09-AUG-2002 (first entry)
XX
DE Murine dual-specificity phosphatase 15 (DSP-15) cDNA.
XX
KW Murine; dual-specificity phosphatase 15; DSP15; antiallergic; cytostatic;
KW immunosuppressive; MAP; mitogen activated protein kinase; cancer; enzyme;
KW signal transduction; cell proliferation; Duchenne muscular dystrophy;
KW cell cycle abnormality; graft-versus-host disease; autoimmune disease;
KW metabolic disease; allergy; screening; gene; ss.
XX
OS Mus musculus.
XX

```
FH   Key             Location/Qualifiers
FT   CDS             35..1450
FT                   /*tag= a
FT                   /product= "Murine DSP-15 protein"
XX
PN   WO200224740-A2.
XX
PD   28-MAR-2002.
XX
PF   19-SEP-2001; 2001WO-US29406.
XX
PR   19-SEP-2000; 2000US-233833P.
PR   18-SEP-2001; 2001US-0955732.
XX
PA   (CEPT-) CEPTYR INC.
XX
PI   Luche RM,  Wei B;
XX
DR   WPI; 2002-394127/42.
DR   P-PSDB; AAE22733.
XX
PT   New dual-specificity phosphatase 15 polypeptide and polynucleotides,
PT   useful for treating e.g. Duchenne muscular dystrophy, cancer,
PT   graft-versus-host disease, autoimmune diseases, allergies, metabolic
PT   diseases
XX
PS   Claim 56; Fig 4; 91pp; English.
XX
CC   The invention relates to a new isolated dual-specificity phosphatase 15
CC   (DSP-15) polypeptide which retains the ability to dephosphorylate an
CC   activated MAP (mitogen activated protein) kinase. DSPs are phosphatases
CC   that dephosphorylate both phosphotyrosine and phosphothreonine/serine
CC   residues. DSP-15 polypeptides may be used to identify agents that
CC   modulate DSP-15 activity, where such agents may inhibit or enhance signal
CC   transduction via a MAP-kinase cascade, leading to cell proliferation. DSP
CC   polypeptides, modulating agents, and/or polynucleotides encoding the
CC   polypeptides may be used to modulate DSP-15 activity in a patient, and to
CC   ameliorate disorders such as Duchenne muscular dystrophy, cancer, graft-
CC   versus-host disease, autoimmune diseases, allergies, metabolic diseases,
CC   abnormal cell growth, abnormal cell proliferation and cell cycle
CC   abnormalities. DSP-15 alternate form polypeptides are useful in screening
CC   assays for modulators of enzyme activity and/or substrate binding. The
CC   present sequence is murine DSP-15 cDNA.
XX
SQ   Sequence 2618 BP; 538 A; 857 C; 769 G; 454 T; 0 other;
```

Alignment Scores:

Pred. No.:	4.51e-195	Length:	2618
Score:	2436.00	Matches:	471
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-761-640-4 (1-471) x AAD36063 (1-2618)

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Qy      1 MetAlaLeuValThrValSerArgSerProProGlySerGlyAlaSerThrProValGly 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     35 ATGGCCCTGGTCACAGTGAGCCGTTCGCCCCCGGGCAGCGGCGCCTCCACGCCCGTGGCG 94

Qy     21 ProTrpAspGlnAlaValGlnArgArgSerArgLeuGlnArgArgGlnSerPheAlaVal 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     95 CCCTGGGACCAGGCGGTCCAGCGAAGGAGTCGACTCCAGCGAAGGCAGAGCTTTGCGGTG 154

Qy     41 LeuArgGlyAlaValLeuGlyLeuGlnAspGlyGlyAspAsnAspAspAlaAlaGluAla 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    155 CTCCGTGGGGCTGTCCTGGGACTGCAGGATGGAGGGGACAATGATGATGCAGCAGAGGCC 214

Qy     61 SerSerGluProThrGluLysAlaProSerGluGluGluLeuHisGlyAspGlnThrAsp 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    215 AGTTCTGAGCCAACAGAGAAGGCCCCGAGTGAGGAGGAGCTCCACGGGGACCAGACAGAC 274

Qy     81 PheGlyGlnGlySerGlnSerProGlnLysGlnGluGluGlnArgGlnHisLeuHisLeu 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    275 TTCGGGCAAGGATCCCAGAGTCCCCAGAAGCAGGAGGAGCAGAGGCAGCACCTGCACCTC 334

Qy    101 MetValGlnLeuLeuArgProGlnAspAspIleArgLeuAlaAlaGlnLeuGluAlaPro 120
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Db    335 ATGGTACAGCTGCTGAGGCCGCAGGATGACATCCGCCTGGCAGCCCAGCTGGAGGCACCC 394

Qy    121 ArgProProArgLeuArgTyrLeuLeuValValSerThrArgGluGlyGluGlyLeuSer 140
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Db    395 CGGCCTCCCCGGCTCCGCTACCTGCTGGTAGTTTCTACACGAGAAGGAGAAGGTCTGAGC 454

Qy    141 GlnAspGluThrValLeuLeuGlyValAspPheProAspSerSerSerProSerCysThr 160
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Db    455 CAGGATGAGACGGTCCTCCTGGGCGTGGATTTCCCTGACAGCAGCTCCCCCAGCTGCACC 514

Qy    161 LeuGlyLeuValLeuProLeuTrpSerAspThrGlnValTyrLeuAspGlyAspGlyGly 180
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Db    515 CTGGGCCTGGTCTTGCCCCTCTGGAGTGACACCCAGGTGTACTTAGATGGAGACGGGGGC 574

Qy    181 PheSerValThrSerGlyGlyGlnSerArgIlePheLysProIleSerIleGlnThrMet 200
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Db    575 TTCAGCGTGACGTCTGGTGGGCAAAGCCGGATCTTCAAGCCCATCTCCATCCAGACCATG 634

Qy    201 TrpAlaThrLeuGlnValLeuHisGlnAlaCysGluAlaAlaLeuGlySerGlyLeuVal 220
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Qy    221 ProGlySerAlaLeuThrTrpAlaSerHisTyrGlnGluArgLeuAsnSerGluGln 240
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Db    695 CCGGGTGGCAGTGCCCTCACCTGGGCCAGCCACTACCAGGAGAGACTGAACTCCGAACAG 754

Qy    241 SerCysLeuAsnGluTrpThrAlaMetAlaAspLeuGluSerLeuArgProProSerAla 260
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Db    755 AGCTGCCTCAATGAGTGGACGGCTATGGCCGACCTGGAGTCTCTGCGGCCTCCCAGCGCC 814

Qy    261 GluProGlyGlySerSerGluGlnGluGlnMetGluGlnAlaIleArgAlaGluLeuTrp 280
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Db    815 GAGCCTGGCGGGTCCTCAGAACAGGAGCAGATGGAGCAGGCGATCCGTGCTGAGCTGTGG 874

Qy    281 LysValLeuAspValSerAspLeuGluSerValThrSerLysGluIleArgGlnAlaLeu 300
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Qy    301 GluLeuArgLeuGlyLeuProLeuGlnGlnTyrArgAspPheIleAspAsnGlnMetLeu 320
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Db    935 GAGCTGCGCCTGGGGCTCCCCCTCCAGCAGTACCGTGACTTCATCGACAACCAGATGCTG 994

Qy    321 LeuLeuValAlaGlnArgAspArgAlaSerArgIlePheProHisLeuTyrLeuGlySer 340
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Db    995 CTGCTGGTGGCACAGCGGGACCGAGCCTCCCGCATCTTCCCCCACCTCTACCTGGGCTCA 1054

Qy    341 GluTrpAsnAlaAlaAsnLeuGluGluLeuGlnArgAsnArgValThrHisIleLeuAsn 360
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Db   1055 GAGTGGAACGCAGCAAACCTGGAGGAGCTGCAGAGGAACAGGGTCACCCACATCTTGAAC 1114

Qy    361 MetAlaArgGluIleAspAsnPheTyrProGluArgPheThrTyrHisAsnValArgLeu 380
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Qy    381 TrpAspGluGluSerAlaGlnLeuLeuProHisTrpLysGluThrHisArgPheIleGlu 400
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Db   1175 TGGGATGAGGAGTCGGCCCAGCTGCTGCCGCACTGGAAGGAGACGCACCGCTTCATTGAG 1234

Qy    401 AlaAlaArgAlaGlnGlyThrHisValLeuValHisCysLysMetGlyValSerArgSer 420
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Db   1235 GCTGCAAGAGCACAGGGCACCCACGTGCTGGTCCACTGCAAGATGGGCGTCAGCCGCTCA 1294

Qy    421 AlaAlaThrValLeuAlaTyrAlaMetLysGlnTyrGluCysSerLeuGluGlnAlaLeu 440
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Db   1295 GCGGCCACAGTGCTGGCCTATGCCATGAAGCAGTACGAATGCAGCCTGGAGCAGGCCCTG 1354

Qy    441 ArgHisValGlnGluLeuArgProIleAlaArgProAsnProGlyPheLeuArgGlnLeu 460
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Db   1355 CGCCACGTGCAGGAGCTCCGGCCCATCGCCCGCCCCAACCCTGGCTTCCTGCGCCAGCTG 1414

Qy    461 GlnIleTyrGlnGlyIleLeuThrAlaArgThr 471
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Db   1415 CAGATCTACCAGGGCATCCTGACGGCCAGAACC 1447

RESULT 2
ABQ73249
ID   ABQ73249 standard; cDNA; 2704 BP.
XX
AC   ABQ73249;
XX
DT   30-SEP-2002  (first entry)
XX
DE   Human MAP kinase phosphatase splice form 1 cDNA sequence SEQ ID NO:1.
XX
KW   Human; phosphatase; mitogen activated protein kinase phosphatase;
KW   MAP kinase; enzyme; chromosome 11; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..93
FT                   /*tag= a
FT   CDS             94..1509
FT                   /*tag= b
FT                   /product= "MAP kinase phosphatase splice form 1"
FT   3'UTR           1510..2704
FT                   /*tag= c
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PN   WO200242436-A2.
XX
PD   30-MAY-2002.
XX
PF   07-NOV-2001; 2001WO-US42995.
XX
PR   20-NOV-2000; 2000US-0715177.
PR   18-JAN-2001; 2001US-0761640.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Wei M, Ketchum KA, Di Francesco V, Beasley EM;
XX
DR   WPI; 2002-575237/61.
DR   P-PSDB; ABP51653.
XX
PT   Novel isolated human phosphatase peptide useful for treating disorder
PT   characterized by absence of, inappropriate or unwanted expression of
PT   the phosphatase protein, and as immunogens to raise antibodies -
XX
PS   Claim 1; Fig 1A; 85pp; English.
XX
CC   The present invention describes an isolated human phosphatase peptide
CC   (I). (I) can be used for identifying a modulator of (I) by contacting
CC   (I) with an agent and determining if the agent has modulated the
CC   function or activity of (I). (I) is useful for identifying an agent that
CC   binds to (I), by contacting (I) with an agent and assaying the contacted
CC   mixture to determine whether a complex is formed with the agent bound
CC   (I). The human phosphatases from the present invention are mitogen
CC   activated protein (MAP) kinase phosphatases. These human MAP kinase
CC   phosphatases are located on chromosome 11. (I) and the polynucleotide
CC   sequences encoding (I) can be used in gene therapy. The present sequence
CC   encodes human MAP kinase phosphatase splice form 1 from the present
CC   invention.
XX
SQ   Sequence 2704 BP; 569 A; 874 C; 794 G; 467 T; 0 other;

Alignment Scores:
Pred. No.:              4.71e-195      Length:          2704
Score:                  2436.00        Matches:         471
Percent Similarity:     100.00%        Conservative:    0
Best Local Similarity:  100.00%        Mismatches:      0
Query Match:            100.00%        Indels:          0

DB:                     24             Gaps:            0

US-09-761-640-4 (1-471) x ABQ73249 (1-2704)

Qy      1 MetAlaLeuValThrValSerArgSerProProGlySerGlyAlaSerThrProValGly 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     94 ATGGCCCTGGTCACAGTGAGCCGTTCGCCCCCGGGCAGCGGCGCCTCCACGCCCGTGGGG 153

Qy     21 ProTrpAspGlnAlaValGlnArgArgSerArgLeuGlnArgArgGlnSerPheAlaVal 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    154 CCCTGGGACCAGGCGGTCCAGCGAAGGAGTCGACTCCAGCGAAGGCAGAGCTTTGCGGTG 213

Qy     41 LeuArgGlyAlaValLeuGlyLeuGlnAspGlyGlyAspAsnAspAspAlaAlaGluAla 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 CTCCGTGGGGCTGTCCTGGGACTGCAGGATGGAGGGGACAATGATGATGCAGCAGAGGCC 273

Qy     61 SerSerGluProThrGluLysAlaProSerGluGluGluLeuHisGlyAspGlnThrAsp 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 AGTTCTGAGCCAACAGAGAAGGCCCCGAGTGAGGAGGAGCTCCACGGGGACCAGACAGAC 333

Qy     81 PheGlyGlnGlySerGlnSerProGlnLysGlnGluGluGlnArgGlnHisLeuHisLeu 100
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Db    334 TTCGGGCAAGGATCCCAGAGTCCCCAGAAGCAGGAGGAGCAGAGGCAGCACCTGCACCTC 393

Qy    101 MetValGlnLeuLeuArgProGlnAspAspIleArgLeuAlaAlaGlnLeuGluAlaPro 120
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Db    394 ATGGTACAGCTGCTGAGGCCGCAGGATGACATCCGCCTGGCAGCCCAGCTGGAGGCACCC 453

Qy    121 ArgProProArgLeuArgTyrLeuLeuValValSerThrArgGluGlyGluGlyLeuSer 140
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Db    454 CGGCCTCCCCGGCTCCGCTACCTGCTGGTAGTTTCTACACGAGAAGGAGAAGGTCTGAGC 513

Qy    141 GlnAspGluThrValLeuLeuGlyValAspPheProAspSerSerSerProSerCysThr 160
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Qy    161 LeuGlyLeuValLeuProLeuTrpSerAspThrGlnValTyrLeuAspGlyAspGlyGly 180
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Qy    181 PheSerValThrSerGlyGlyGlnSerArgIlePheLysProIleSerIleGlnThrMet 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 TTCAGCGTGACGTCTGGTGGGCAAAGCCGGATCTTCAAGCCCATCTCCATCCAGACCATG 693

Qy    201 TrpAlaThrLeuGlnValLeuHisGlnAlaCysGluAlaAlaLeuGlySerGlyLeuVal 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 TGGGCCACACTCCAGGTATTGCACCAAGCATGTGAGGCAGCTCTAGGCAGCGGCCTTGTA 753

Qy    221 ProGlyGlySerAlaLeuThrTrpAlaSerHisTyrGlnGluArgLeuAsnSerGluGln 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 CCGGGTGGCAGTGCCCTCACCTGGGCCAGCCACTACCAGGAGAGACTGAACTCCGAACAG 813

Qy    241 SerCysLeuAsnGluTrpThrAlaMetAlaAspLeuGluSerLeuArgProProSerAla 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 AGCTGCCTCAATGAGTGGACGGCTATGGCCGACCTGGAGTCTCTGCGGCCTCCCAGCGCC 873

Qy    261 GluProGlyGlySerSerGluGlnGluGlnMetGluGlnAlaIleArgAlaGluLeuTrp 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 GAGCCTGGCGGGTCCTCAGAACAGGAGCAGATGGAGCAGGCGATCCGTGCTGAGCTGTGG 933

Qy    281 LysValLeuAspValSerAspLeuGluSerValThrSerLysGluIleArgGlnAlaLeu 300
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Db    934 AAAGTGTTGGATGTCAGTGACCTGGAGAGTGTCACTTCCAAAGAGATCCGCCAGGCTCTG 993

Qy    301 GluLeuArgLeuGlyLeuProLeuGlnGlnTyrArgAspPheIleAspAsnGlnMetLeu 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 GAGCTGCGCCTGGGGCTCCCCCTCCAGCAGTACCGTGACTTCATCGACAACCAGATGCTG 1053

Qy    321 LeuLeuValAlaGlnArgAspArgAlaSerArgIlePheProHisLeuTyrLeuGlySer 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 CTGCTGGTGGCACAGCGGGACCGAGCCTCCCGCATCTTCCCCCACCTCTACCTGGGCTCA 1113

Qy    341 GluTrpAsnAlaAlaAsnLeuGluGluLeuGlnArgAsnArgValThrHisIleLeuAsn 360
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